

SEQUENCE LISTING

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 Hoeger, Thomas
 Kroeger, Burkhard
 Otterbach, Bernd
 Lubisch, Wilfried
 Lemaire, Hans-Georg

<120> Poly (ADP-ribose) polymerase-gene

<130> 0050/49100

<140> US 09/701,586

<141> 2000-11-30

<150> PCT/EP99/03889

<151> 1999-06-04

<160> 33

<170> PatentIn/WordPerfect

<210> 1

<211> 1843

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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<223> product is Poly ADP Ribose Polymerase; from brain tissue

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 Ala Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu
 20 25 30

gac tct tcc cct gcc aag aaa act cgt aga tgc cag aga cag gag tcg 143
 Asp Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser
 35 40 45

aaa aag atg cct gtg gct gga gga aaa gct aat aag gac agg aca gaa 191
 Lys Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu
 50 55 60

gac aag caa gat gaa tct gtg aag gcc ttg ctg tta aag ggc aaa gct 239
 Asp Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Lys Gly Lys Ala

Sub
C4

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Pro Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr			
80	85	90	95
tgt gaa gga aat gat gtc tat gat gtc atg cta aat cag acc aat ctc			335
Cys Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu			
	100	105	110
cag ttc aac aac aac aag tac tat ctg att cag cta tta gaa gat gat			383
Gln Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp			
	115	120	125
gcc cag agg aac ttc agt gtt tgg atg aga tgg ggc cga gtt ggg aaa			431
Ala Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys			
	130	135	140
atg gga cag cac agc ctg gtg gct tgt tca ggc aat ctc aac aag gcc			479
Met Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala			
	145	150	155
aag gaa atc ttt cag aag aaa ttc ctt gac aaa acg aaa aac aat tgg			527
Lys Glu Ile Phe Gln Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp			
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gaa gat cga gaa aag ttt gag aag gtg cct gga aaa tat gat atg cta			575
Glu Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu			
	180	185	190
cag atg gac tat gcc acc aat act cag gat gaa gag gaa aca aag aaa			623
Gln Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Glu Thr Lys Lys			
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gag gaa tct ctt aaa tct ccc ttg aag cca gag tca cag cta gat ctt			671
Glu Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu			
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cgg gta cag gag tta ata aag ttg atc tgt aat gtt cag gcc atg gaa			719
Arg Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu			
	225	230	235
gaa atg atg atg gaa atg aag tat aat acc aag aaa gcc cca ctt ggg			767
Glu Met Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly			
240	245	250	255
aag ctg aca gtg gca caa atc aag gca ggt tac cag tct ctt aag aag			815
Lys Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys			
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att gag gat tgt att cgg gct ggc cag cat gga cga gct ctc atg gaa			863
Ile Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu			
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Thr Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln	
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tta cta gag gct ttg gga gac att gaa att gct att aag ctg gtg aaa	1007
Leu Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys	
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Thr Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn	
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Leu His Cys Ala Leu Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys	
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gtg att tcc cag tac cta caa tct acc cat gct ccc aca cac agc gac	1151
Val Ile Ser Gln Tyr Leu Gln Ser Thr His Ala Pro Thr His Ser Asp	
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Tyr Thr Met Thr Leu Leu Asp Leu Phe Glu Val Glu Lys Asp Gly Glu	
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Lys Glu Ala Phe Arg Glu Asp Leu His Asn Arg Met Leu Leu Trp His	
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Gly Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg	
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Ile Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly	
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Ile Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala	
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tct cgc cta aag aat aca gga ctg ctg ctc tta tca gag gta gct cta	1439
Ser Arg Leu Lys Asn Thr Gly Leu Leu Leu Leu Ser Glu Val Ala Leu	
465 470 475	
ggt cag tgt aat gaa cta cta gag gcc aat cct aag gcc gaa gga ttg	1487
Gly Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu	
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ctt caa ggt aaa cat agc acc aag ggg ctg ggc aag atg gct ccc agt	1535

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Ser	Ala	His	Phe	Val	Thr	Leu	Asn	Gly	Ser	Thr	Val	Pro	Leu	Gly	Pro		
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Ala	Ser	Asp	Thr	Gly	Ile	Leu	Asn	Pro	Asp	Gly	Tyr	Thr	Leu	Asn	Tyr		
			530				535					540					
aat	gaa	tat	att	gta	tat	aac	ccc	aac	cag	gtc	cgt	atg	cgg	tac	ctt		1679
Asn	Glu	Tyr	Ile	Val	Tyr	Asn	Pro	Asn	Gln	Val	Arg	Met	Arg	Tyr	Leu		
	545					550					555						
tta	aag	gtt	cag	ttt	aat	ttc	ctt	cag	ctg	tgg	tga	atgttgatat					1725
Leu	Lys	Val	Gln	Phe	Asn	Phe	Leu	Gln	Leu	Trp	*						
560					565					570							
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Lys	Gln	Asp	Glu	Ser	Val	Lys	Ala	Leu	Leu	Leu	Lys	Gly	Lys	Ala	Pro		
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Val	Asp	Pro	Glu	Cys	Thr	Ala	Lys	Val	Gly	Lys	Ala	His	Val	Tyr	Cys		
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Glu	Gly	Asn	Asp	Val	Tyr	Asp	Val	Met	Leu	Asn	Gln	Thr	Asn	Leu	Gln		
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Phe	Asn	Asn	Asn	Lys	Tyr	Tyr	Leu	Ile	Gln	Leu	Leu	Glu	Asp	Asp	Ala		
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Gln	Arg	Asn	Phe	Ser	Val	Trp	Met	Arg	Trp	Gly	Arg	Val	Gly	Lys	Met	130	135	140	
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Glu	Ile	Phe	Gln	Lys	Lys	Phe	Leu	Asp	Lys	Thr	Lys	Asn	Asn	Trp	Glu	165	170	175	
Asp	Arg	Glu	Lys	Phe	Glu	Lys	Val	Pro	Gly	Lys	Tyr	Asp	Met	Leu	Gln	180	185	190	
Met	Asp	Tyr	Ala	Thr	Asn	Thr	Gln	Asp	Glu	Glu	Glu	Thr	Lys	Lys	Glu	195	200	205	
Glu	Ser	Leu	Lys	Ser	Pro	Leu	Lys	Pro	Glu	Ser	Gln	Leu	Asp	Leu	Arg	210	215	220	
Val	Gln	Glu	Leu	Ile	Lys	Leu	Ile	Cys	Asn	Val	Gln	Ala	Met	Glu	Glu	225	230	235	240
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Glu	Asp	Cys	Ile	Arg	Ala	Gly	Gln	His	Gly	Arg	Ala	Leu	Met	Glu	Ala	275	280	285	
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Pro	Pro	Leu	Ile	Arg	Thr	Gln	Lys	Glu	Leu	Ser	Glu	Lys	Ile	Gln	Leu	305	310	315	320
Leu	Glu	Ala	Leu	Gly	Asp	Ile	Glu	Ile	Ala	Ile	Lys	Leu	Val	Lys	Thr	325	330	335	
Glu	Leu	Gln	Ser	Pro	Glu	His	Pro	Leu	Asp	Gln	His	Tyr	Arg	Asn	Leu	340	345	350	
His	Cys	Ala	Leu	Arg	Pro	Leu	Asp	His	Glu	Ser	Tyr	Glu	Phe	Lys	Val	355	360	365	
Ile	Ser	Gln	Tyr	Leu	Gln	Ser	Thr	His	Ala	Pro	Thr	His	Ser	Asp	Tyr	370	375	380	
Thr	Met	Thr	Leu	Leu	Asp	Leu	Phe	Glu	Val	Glu	Lys	Asp	Gly	Glu	Lys	385	390	395	400
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 Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly Ile
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 465 470 475 480
 Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu Leu
 485 490 495
 Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser Ser
 500 505 510
 Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro Ala
 515 520 525
 Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr Asn
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<212> DNA

<213> Homo sapiens

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<223> product is Poly ADP Ribose Polymerase; from uterus tissue

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TCTCCCTAAT TCACGCCTGA GGCTCATGGA GAGTTGCTAG ACCTGGGACT GCCCTGGGAG	180
GCGCACACAA CCAGGCCGGG TGGCAGCCAG GACCTCTCCC ATGTCCCTGC TTTTCTTGGC	240
C ATG GCT CCA AAG CCG AAG CCC TGG GTA CAG ACT GAG GGC CCT GAG	286
Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu	

575						580						585						
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Lys	Lys	Lys	Gly	Arg	Gln	Ala	Gly	Arg	Glu	Glu	Asp	Pro	Phe	Arg	Ser			
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ACC	GCT	GAG	GCC	CTC	AAG	GCC	ATA	CCC	GCA	GAG	AAG	CGC	ATA	ATC	CGC	382		
Thr	Ala	Glu	Ala	Leu	Lys	Ala	Ile	Pro	Ala	Glu	Lys	Arg	Ile	Ile	Arg			
			605						610			615						
GTG	GAT	CCA	ACA	TGT	CCA	CTC	AGC	AGC	AAC	CCC	GGG	ACC	CAG	GTG	TAT	430		
Val	Asp	Pro	Thr	Cys	Pro	Leu	Ser	Ser	Asn	Pro	Gly	Thr	Gln	Val	Tyr			
			620						625			630						
GAG	GAC	TAC	AAC	TGC	ACC	CTG	AAC	CAG	ACC	AAC	ATC	GAG	AAC	AAC	AAC	478		
Glu	Asp	Tyr	Asn	Cys	Thr	Leu	Asn	Gln	Thr	Asn	Ile	Glu	Asn	Asn	Asn			
635						640						645			650			
AAC	AAG	TTC	TAC	ATC	ATC	CAG	CTG	CTC	CAA	GAC	AGC	AAC	CGC	TTC	TTC	526		
Asn	Lys	Phe	Tyr	Ile	Ile	Gln	Leu	Leu	Gln	Asp	Ser	Asn	Arg	Phe	Phe			
			655						660			665						
ACC	TGC	TGG	AAC	CGC	TGG	GGC	CGT	GTG	GGA	GAG	GTC	GGC	CAG	TCA	AAG	574		
Thr	Cys	Trp	Asn	Arg	Trp	Gly	Arg	Val	Gly	Glu	Val	Gly	Gln	Ser	Lys			
			670						675			680						
ATC	AAC	CAC	TTC	ACA	AGG	CTA	GAA	GAT	GCA	AAG	AAG	GAC	TTT	GAG	AAG	622		
Ile	Asn	His	Phe	Thr	Arg	Leu	Glu	Asp	Ala	Lys	Lys	Asp	Phe	Glu	Lys			
			685						690			695						
AAA	TTT	CGG	GAA	AAG	ACC	AAG	AAC	AAC	TGG	GCA	GAG	CGG	GAC	CAC	TTT	670		
Lys	Phe	Arg	Glu	Lys	Thr	Lys	Asn	Asn	Trp	Ala	Glu	Arg	Asp	His	Phe			
			700						705			710						
GTG	TCT	CAC	CCG	GGC	AAG	TAC	ACA	CTT	ATC	GAA	GTA	CAG	GCA	GAG	GAT	718		
Val	Ser	His	Pro	Gly	Lys	Tyr	Thr	Leu	Ile	Glu	Val	Gln	Ala	Glu	Asp			
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GAG	GCC	CAG	GAA	GCT	GTG	GTG	AAG	GTG	GAC	AGA	GGC	CCA	GTG	AGG	ACT	766		
Glu	Ala	Gln	Glu	Ala	Val	Val	Lys	Val	Asp	Arg	Gly	Pro	Val	Arg	Thr			
			735						740			745						
GTG	ACT	AAG	CGG	GTG	CAG	CCC	TGC	TCC	CTG	GAC	CCA	GCC	ACG	CAG	AAG	814		
Val	Thr	Lys	Arg	Val	Gln	Pro	Cys	Ser	Leu	Asp	Pro	Ala	Thr	Gln	Lys			
			750						755			760						
CTC	ATC	ACT	AAC	ATC	TTC	AGC	AAG	GAG	ATG	TTC	AAG	AAC	ACC	ATG	GCC	862		
Leu	Ile	Thr	Asn	Ile	Phe	Ser	Lys	Glu	Met	Phe	Lys	Asn	Thr	Met	Ala			
			765						770			775						
CTC	ATG	GAC	CTG	GAT	GTG	AAG	AAG	ATG	CCC	CTG	GGA	AAG	CTG	AGC	AAG	910		
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CTG AAA GGC CCC ACG GAT GGT GGC CAA AGC CTG GAG GAG CTG TCC TCA	1006
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CAC TTT TAC ACC GTC ATC CCG CAC AAC TTC GGC CAC AGC CAG CCC CCG	1054
His Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro Pro	
830 835 840	
CCC ATC AAT TCC CCT GAG CTT CTG CAG GCC AAG AAG GAC ATG CTG CTG	1102
Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu Leu	
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GTG CTG GCG GAC ATC GAG CTG GCC CAG GCC CTG CAG GCA GTC TCT GAG	1150
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860 865 870	
CAG GAG AAG ACG GTG GAG GAG GTG CCA CAC CCC CTG GAC CGA GAC TAC	1198
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875 880 885 890	
CAG CTT CTC AAG TGC CAG CTG CAG CTG CTA GAC TCT GGA GCA CCT GAG	1246
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TAC AAG GTG ATA CAG ACC TAC TTA GAA CAG ACT GGC AGC AAC CAC AGG	1294
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Cys Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu Glu	
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GAC AGA TTC CAG GCC CAC TCC AAA CTG GGT AAT CGG AAG CTG CTG TGG	1390
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His Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu	
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GCC TCA GAG AAC AGC AAG TCA GCT GGA TAT GTT ATT GGC ATG AAG TGT	1534
Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys Cys	
990 995 1000	
GGG GCC CAC CAT GTC GGC TAC ATG TTC CTG GGT GAG GTG GCC CTG GGC	1582

Gly Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly
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 AGA GAG CAC CAT ATC AAC ACG GAC AAC CCC AGC TTG AAG AGC CCA CCT 1630
 Arg Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro
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 Pro Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro
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 Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro
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 CAG GGC CAG CCT GTG CCC TGC CCA GAG TTC AGC AGC TCC ACA TTC TCC 1774
 Gln Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser
 1070 1075 1080
 CAG AGC GAG TAC CTC ATC TAC CAG GAG AGC CAG TGT CGC CTG CGC TAC 1822
 Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg Tyr
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 Leu Leu Glu Val His Leu *
 1100 1105
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 <212> PRT
 <213> Homo sapiens

<400> 4

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Asp	Pro	Thr	Cys	Pro	Leu	Ser	Ser	Asn	Pro	Gly	Thr	Gln	Val	Tyr	Glu	50	55	60	
Asp	Tyr	Asn	Cys	Thr	Leu	Asn	Gln	Thr	Asn	Ile	Glu	Asn	Asn	Asn	Asn	65	70	75	80
Lys	Phe	Tyr	Ile	Ile	Gln	Leu	Leu	Gln	Asp	Ser	Asn	Arg	Phe	Phe	Thr	85	90	95	
Cys	Trp	Asn	Arg	Trp	Gly	Arg	Val	Gly	Glu	Val	Gly	Gln	Ser	Lys	Ile	100	105	110	
Asn	His	Phe	Thr	Arg	Leu	Glu	Asp	Ala	Lys	Lys	Asp	Phe	Glu	Lys	Lys	115	120	125	
Phe	Arg	Glu	Lys	Thr	Lys	Asn	Asn	Trp	Ala	Glu	Arg	Asp	His	Phe	Val	130	135	140	
Ser	His	Pro	Gly	Lys	Tyr	Thr	Leu	Ile	Glu	Val	Gln	Ala	Glu	Asp	Glu	145	150	155	160
Ala	Gln	Glu	Ala	Val	Val	Lys	Val	Asp	Arg	Gly	Pro	Val	Arg	Thr	Val	165	170	175	
Thr	Lys	Arg	Val	Gln	Pro	Cys	Ser	Leu	Asp	Pro	Ala	Thr	Gln	Lys	Leu	180	185	190	
Ile	Thr	Asn	Ile	Phe	Ser	Lys	Glu	Met	Phe	Lys	Asn	Thr	Met	Ala	Leu	195	200	205	
Met	Asp	Leu	Asp	Val	Lys	Lys	Met	Pro	Leu	Gly	Lys	Leu	Ser	Lys	Gln	210	215	220	
Gln	Ile	Ala	Arg	Gly	Phe	Glu	Ala	Leu	Glu	Ala	Leu	Glu	Glu	Ala	Leu	225	230	235	240
Lys	Gly	Pro	Thr	Asp	Gly	Gly	Gln	Ser	Leu	Glu	Glu	Leu	Ser	Ser	His	245	250	255	
Phe	Tyr	Thr	Val	Ile	Pro	His	Asn	Phe	Gly	His	Ser	Gln	Pro	Pro	Pro	260	265	270	
Ile	Asn	Ser	Pro	Glu	Leu	Leu	Gln	Ala	Lys	Lys	Asp	Met	Leu	Leu	Val	275	280	285	
Leu	Ala	Asp	Ile	Glu	Leu	Ala	Gln	Ala	Leu	Gln	Ala	Val	Ser	Glu	Gln	290	295	300	
Glu	Lys	Thr	Val	Glu	Glu	Val	Pro	His	Pro	Leu	Asp	Arg	Asp	Tyr	Gln	305	310	315	320

Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro Glu Tyr
 325 330 335
 Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His Arg Cys
 340 345 350
 Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu Glu Asp
 355 360 365
 Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu Trp His
 370 375 380
 Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg
 385 390 395 400
 Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala
 405 410 415
 Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys Cys Gly
 420 425 430
 Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Arg
 435 440 445
 Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro Pro
 450 455 460
 Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro Thr
 465 470 475 480
 Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro Gln
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 Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser Gln
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<211> 2265

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 221..1843

<223> product is Poly ADP Ribose Polymerase; from uterus tissue

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TCTCCCTAAT	TCACGCCTGA	GGCTCATGGA	GAGTTGCTAG	ACCTGGGACT	GCCCTGGGAG	180										
GCGCACACAA	CCAGGCCGGG	TGGCAGCCAG	GACCTCTCCC	ATG	TCC CTG CTT TTC	235										
				Met	Ser Leu Leu Phe	535										
TTG	GCC	ATG	GCT	CCA	AAG	CCG	AAG	CCC	TGG	GTA	CAG	ACT	GAG	GGC	CCT	283
Leu	Ala	Met	Ala	Pro	Lys	Pro	Lys	Pro	Trp	Val	Gln	Thr	Glu	Gly	Pro	540
540					545				550						555	
GAG	AAG	AAG	AAG	GGC	CGG	CAG	GCA	GGA	AGG	GAG	GAG	GAC	CCC	TTC	CGC	331
Glu	Lys	Lys	Lys	Gly	Arg	Gln	Ala	Gly	Arg	Glu	Glu	Asp	Pro	Phe	Arg	560
				560				565						570		
TCC	ACC	GCT	GAG	GCC	CTC	AAG	GCC	ATA	CCC	GCA	GAG	AAG	CGC	ATA	ATC	379
Ser	Thr	Ala	Glu	Ala	Leu	Lys	Ala	Ile	Pro	Ala	Glu	Lys	Arg	Ile	Ile	575
			575				580						585			
CGC	GTG	GAT	CCA	ACA	TGT	CCA	CTC	AGC	AGC	AAC	CCC	GGG	ACC	CAG	GTG	427
Arg	Val	Asp	Pro	Thr	Cys	Pro	Leu	Ser	Ser	Asn	Pro	Gly	Thr	Gln	Val	590
		590					595					600				
TAT	GAG	GAC	TAC	AAC	TGC	ACC	CTG	AAC	CAG	ACC	AAC	ATC	GAG	AAC	AAC	475
Tyr	Glu	Asp	Tyr	Asn	Cys	Thr	Leu	Asn	Gln	Thr	Asn	Ile	Glu	Asn	Asn	605
	605				610						615					
AAC	AAC	AAG	TTC	TAC	ATC	ATC	CAG	CTG	CTC	CAA	GAC	AGC	AAC	CGC	TTC	523
Asn	Asn	Lys	Phe	Tyr	Ile	Ile	Gln	Leu	Leu	Gln	Asp	Ser	Asn	Arg	Phe	620
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TTC	ACC	TGC	TGG	AAC	CGC	TGG	GGC	CGT	GTG	GGA	GAG	GTC	GGC	CAG	TCA	571
Phe	Thr	Cys	Trp	Asn	Arg	Trp	Gly	Arg	Val	Gly	Glu	Val	Gly	Gln	Ser	640
				640				645						650		
AAG	ATC	AAC	CAC	TTC	ACA	AGG	CTA	GAA	GAT	GCA	AAG	AAG	GAC	TTT	GAG	619
Lys	Ile	Asn	His	Phe	Thr	Arg	Leu	Glu	Asp	Ala	Lys	Lys	Asp	Phe	Glu	655
			655					660					665			
AAG	AAA	TTT	CGG	GAA	AAG	ACC	AAG	AAC	AAC	TGG	GCA	GAG	CGG	GAC	CAC	667
Lys	Lys	Phe	Arg	Glu	Lys	Thr	Lys	Asn	Asn	Trp	Ala	Glu	Arg	Asp	His	670
		670					675					680				
TTT	GTG	TCT	CAC	CCG	GGC	AAG	TAC	ACA	CTT	ATC	GAA	GTA	CAG	GCA	GAG	715
Phe	Val	Ser	His	Pro	Gly	Lys	Tyr	Thr	Leu	Ile	Glu	Val	Gln	Ala	Glu	685
	685					690					695					
GAT	GAG	GCC	CAG	GAA	GCT	GTG	GTG	AAG	GTG	GAC	AGA	GGC	CCA	GTG	AGG	763
Asp	Glu	Ala	Gln	Glu	Ala	Val	Val	Lys	Val	Asp	Arg	Gly	Pro	Val	Arg	700
					705					710					715	
ACT	GTG	ACT	AAG	CGG	GTG	CAG	CCC	TGC	TCC	CTG	GAC	CCA	GCC	ACG	CAG	811

Thr	Val	Thr	Lys	Arg	Val	Gln	Pro	Cys	Ser	Leu	Asp	Pro	Ala	Thr	Gln	
				720					725						730	
AAG	CTC	ATC	ACT	AAC	ATC	TTC	AGC	AAG	GAG	ATG	TTC	AAG	AAC	ACC	ATG	859
Lys	Leu	Ile	Thr	Asn	Ile	Phe	Ser	Lys	Glu	Met	Phe	Lys	Asn	Thr	Met	
			735					740					745			
GCC	CTC	ATG	GAC	CTG	GAT	GTG	AAG	AAG	ATG	CCC	CTG	GGA	AAG	CTG	AGC	907
Ala	Leu	Met	Asp	Leu	Asp	Val	Lys	Lys	Met	Pro	Leu	Gly	Lys	Leu	Ser	
		750					755					760				
AAG	CAA	CAG	ATT	GCA	CGG	GGT	TTC	GAG	GCC	TTG	GAG	GCG	CTG	GAG	GAG	955
Lys	Gln	Gln	Ile	Ala	Arg	Gly	Phe	Glu	Ala	Leu	Glu	Ala	Leu	Glu	Glu	
	765					770					775					
GCC	CTG	AAA	GGC	CCC	ACG	GAT	GGT	GGC	CAA	AGC	CTG	GAG	GAG	CTG	TCC	1003
Ala	Leu	Lys	Gly	Pro	Thr	Asp	Gly	Gly	Gln	Ser	Leu	Glu	Glu	Leu	Ser	
780					785					790					795	
TCA	CAC	TTT	TAC	ACC	GTC	ATC	CCG	CAC	AAC	TTC	GGC	CAC	AGC	CAG	CCC	1051
Ser	His	Phe	Tyr	Thr	Val	Ile	Pro	His	Asn	Phe	Gly	His	Ser	Gln	Pro	
			800						805					810		
CCG	CCC	ATC	AAT	TCC	CCT	GAG	CTT	CTG	CAG	GCC	AAG	AAG	GAC	ATG	CTG	1099
Pro	Pro	Ile	Asn	Ser	Pro	Glu	Leu	Leu	Gln	Ala	Lys	Lys	Asp	Met	Leu	
			815					820					825			
CTG	GTG	CTG	GCG	GAC	ATC	GAG	CTG	GCC	CAG	GCC	CTG	CAG	GCA	GTC	TCT	1147
Leu	Val	Leu	Ala	Asp	Ile	Glu	Leu	Ala	Gln	Ala	Leu	Gln	Ala	Val	Ser	
		830					835					840				
GAG	CAG	GAG	AAG	ACG	GTG	GAG	GAG	GTG	CCA	CAC	CCC	CTG	GAC	CGA	GAC	1195
Glu	Gln	Glu	Lys	Thr	Val	Glu	Glu	Val	Pro	His	Pro	Leu	Asp	Arg	Asp	
	845					850					855					
TAC	CAG	CTT	CTC	AAG	TGC	CAG	CTG	CAG	CTG	CTA	GAC	TCT	GGA	GCA	CCT	1243
Tyr	Gln	Leu	Leu	Lys	Cys	Gln	Leu	Gln	Leu	Leu	Asp	Ser	Gly	Ala	Pro	
860					865					870					875	
GAG	TAC	AAG	GTG	ATA	CAG	ACC	TAC	TTA	GAA	CAG	ACT	GGC	AGC	AAC	CAC	1291
Glu	Tyr	Lys	Val	Ile	Gln	Thr	Tyr	Leu	Glu	Gln	Thr	Gly	Ser	Asn	His	
			880						885					890		
AGG	TGC	CCT	ACA	CTT	CAA	CAC	ATC	TGG	AAA	GTA	AAC	CAA	GAA	GGG	GAG	1339
Arg	Cys	Pro	Thr	Leu	Gln	His	Ile	Trp	Lys	Val	Asn	Gln	Glu	Gly	Glu	
			895					900					905			
GAA	GAC	AGA	TTC	CAG	GCC	CAC	TCC	AAA	CTG	GGT	AAT	CGG	AAG	CTG	CTG	1387
Glu	Asp	Arg	Phe	Gln	Ala	His	Ser	Lys	Leu	Gly	Asn	Arg	Lys	Leu	Leu	
		910					915					920				
TGG	CAT	GGC	ACC	AAC	ATG	GCC	GTG	GTG	GCC	GCC	ATC	CTC	ACT	AGT	GGG	1435
Trp	His	Gly	Thr	Asn	Met	Ala	Val	Val	Ala	Ala	Ile	Leu	Thr	Ser	Gly	
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Leu Arg Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr	
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TTT GCC TCA GAG AAC AGC AAG TCA GCT GGA TAT GTT ATT GGC ATG AAG	1531
Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys	
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TGT GGG GCC CAC CAT GTC GGC TAC ATG TTC CTG GGT GAG GTG GCC CTG	1579
Cys Gly Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu	
975 980 985	
GGC AGA GAG CAC CAT ATC AAC ACG GAC AAC CCC AGC TTG AAG AGC CCA	1627
Gly Arg Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro	
990 995 1000	
CCT CCT GGC TTC GAC AGT GTC ATT GCC CGA GGC CAC ACC GAG CCT GAT	1675
Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp	
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CCG ACC CAG GAC ACT GAG TTG GAG CTG GAT GGC CAG CAA GTG GTG GTG	1723
Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val	
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CCC CAG GGC CAG CCT GTG CCC TGC CCA GAG TTC AGC AGC TCC ACA TTC	1771
Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe	
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TCC CAG AGC GAG TAC CTC ATC TAC CAG GAG AGC CAG TGT CGC CTG CGC	1819
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TAC CTG CTG GAG GTC CAC CTC TGA GTGCCCCGCC TGTCCCCCGG GGTCTTGCAA	1873
Tyr Leu Leu Glu Val His Leu *	
1070 1075	
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TTTCAAGAAT ACAATACGTT GTTGTTAACT ATAGTCACCA TGCTGTACAA GATCCCTGAA	1993
CTTATGCCTC CTAAGTAAAA TTTTGTATTC TTTGACACAT CTGCCCAGTC CCTCTCCTCC	2053
CAGCCCATGG TAACCAGCAT TTGACTCTTT ACTTGTATAA GGGCAGCTTT TATAGGTTCC	2113
ACATGTAAGT GAGATCATGC AGTGTGTTGTC TTTCTGTGCC TGGCTTATTT CACTCAGCAT	2173
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<212> PRT

<400> 6

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		20					25						30		
Glu	Asp	Pro	Phe	Arg	Ser	Thr	Ala	Glu	Ala	Leu	Lys	Ala	Ile	Pro	Ala
		35					40					45			
Glu	Lys	Arg	Ile	Ile	Arg	Val	Asp	Pro	Thr	Cys	Pro	Leu	Ser	Ser	Asn
	50					55					60				
Pro	Gly	Thr	Gln	Val	Tyr	Glu	Asp	Tyr	Asn	Cys	Thr	Leu	Asn	Gln	Thr
65					70					75					80
Asn	Ile	Glu	Asn	Asn	Asn	Asn	Lys	Phe	Tyr	Ile	Ile	Gln	Leu	Leu	Gln
				85					90					95	
Asp	Ser	Asn	Arg	Phe	Phe	Thr	Cys	Trp	Asn	Arg	Trp	Gly	Arg	Val	Gly
			100					105					110		
Glu	Val	Gly	Gln	Ser	Lys	Ile	Asn	His	Phe	Thr	Arg	Leu	Glu	Asp	Ala
		115					120					125			
Lys	Lys	Asp	Phe	Glu	Lys	Lys	Phe	Arg	Glu	Lys	Thr	Lys	Asn	Asn	Trp
	130					135					140				
Ala	Glu	Arg	Asp	His	Phe	Val	Ser	His	Pro	Gly	Lys	Tyr	Thr	Leu	Ile
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Glu	Val	Gln	Ala	Glu	Asp	Glu	Ala	Gln	Glu	Ala	Val	Val	Lys	Val	Asp
				165				170						175	
Arg	Gly	Pro	Val	Arg	Thr	Val	Thr	Lys	Arg	Val	Gln	Pro	Cys	Ser	Leu
			180					185					190		
Asp	Pro	Ala	Thr	Gln	Lys	Leu	Ile	Thr	Asn	Ile	Phe	Ser	Lys	Glu	Met
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Phe	Lys	Asn	Thr	Met	Ala	Leu	Met	Asp	Leu	Asp	Val	Lys	Lys	Met	Pro
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Leu	Gly	Lys	Leu	Ser	Lys	Gln	Gln	Ile	Ala	Arg	Gly	Phe	Glu	Ala	Leu
225					230					235					240
Glu	Ala	Leu	Glu	Glu	Ala	Leu	Lys	Gly	Pro	Thr	Asp	Gly	Gly	Gln	Ser
				245					250					255	
Leu	Glu	Glu	Leu	Ser	Ser	His	Phe	Tyr	Thr	Val	Ile	Pro	His	Asn	Phe
			260					265					270		

Gly His Ser Gln Pro Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala
 275 280 285
 Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala
 290 295 300
 Leu Gln Ala Val Ser Glu Gln Glu Lys Thr Val Glu Glu Val Pro His
 305 310 315 320
 Pro Leu Asp Arg Asp Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu
 325 330 335
 Asp Ser Gly Ala Pro Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln
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 Thr Gly Ser Asn His Arg Cys Pro Thr Leu Gln His Ile Trp Lys Val
 355 360 365
 Asn Gln Glu Gly Glu Glu Asp Arg Phe Gln Ala His Ser Lys Leu Gly
 370 375 380
 Asn Arg Lys Leu Leu Trp His Gly Thr Asn Met Ala Val Val Ala Ala
 385 390 395 400
 Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser Gly Gly Arg Val
 405 410 415
 Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr
 420 425 430
 Val Ile Gly Met Lys Cys Gly Ala His His Val Gly Tyr Met Phe Leu
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 Gly Glu Val Ala Leu Gly Arg Glu His His Ile Asn Thr Asp Asn Pro
 450 455 460
 Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly
 465 470 475 480
 His Thr Glu Pro Asp Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly
 485 490 495
 Gln Gln Val Val Val Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe
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 515 520 525
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Met Ala	
CCA AAA CGA AAG GCC TCT GTG CAG ACT GAG GGC TCC AAG AAG CAG CGA	165
Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys Gln Arg	
545 550 555	
CAA GGG ACA GAG GAG GAG GAC AGC TTC CGG TCC ACT GCC GAG GCT CTC	213
Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu Ala Leu	
560 565 570 575	
AGA GCA GCA CCT GCT GAT AAT CGG GTC ATC CGT GTG GAC CCC TCA TGT	261
Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro Ser Cys	
580 585 590	
CCA TTC AGC CGG AAC CCC GGG ATA CAG GTC CAC GAG GAC TAT GAC TGT	309
Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr Asp Cys	
595 600 605	
ACC CTG AAC CAG ACC AAC ATC GGC AAC AAC AAC AAC AAG TTC TAT ATT	357
Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe Tyr Ile	
610 615 620	
ATC CAA CTG CTG GAG GAG GGT AGT CGC TTC TTC TGC TGG AAT CGC TGG	405
Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn Arg Trp	
625 630 635	
GGC CGC GTG GGA GAG GTG GGC CAG AGC AAG ATG AAC CAC TTC ACC TGC	453
Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe Thr Cys	
640 645 650 655	
CTG GAA GAT GCA AAG AAG GAC TTT AAG AAG AAA TTT TGG GAG AAG ACT	501
Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu Lys Thr	
660 665 670	
AAA AAC AAA TGG GAG GAG CGG GAC CGT TTT GTG GCC CAG CCC AAC AAG	549
Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro Asn Lys	
675 680 685	
TAC ACA CTT ATA GAA GTC CAG GGA GAA GCA GAG AGC CAA GAG GCT GTA	597
Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu Ala Val	
690 695 700	

GTG AAG GCC TTA TCT CCC CAG GTG GAC AGC GGC CCT GTG AGG ACC GTG Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg Thr Val 705 710 715	645
GTC AAG CCC TGC TCC CTA GAC CCT GCC ACC CAG AAC CTT ATC ACC AAC Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn 720 725 730 735	693
ATC TTC AGC AAA GAG ATG TTC AAG AAC GCA ATG ACC CTC ATG AAC CTG Ile Phe Ser Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu 740 745 750	741
GAT GTG AAG AAG ATG CCC TTG GGA AAG CTG ACC AAG CAG CAG ATT GCC Asp Val Lys Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala 755 760 765	789
CGT GGC TTC GAG GCC TTG GAA GCT CTA GAG GAG GCC ATG AAA AAC CCC Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro 770 775 780	837
ACA GGG GAT GGC CAG AGC CTG GAA GAG CTC TCC TCC TGC TTC TAC ACT Thr Gly Asp Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr 785 790 795	885
GTC ATC CCA CAC AAC TTC GGC CGC AGC CGA CCC CCG CCC ATC AAC TCC Val Ile Pro His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser 800 805 810 815	933
CCT GAT GTG CTT CAG GCC AAG AAG GAC ATG CTG CTG GTG CTA GCG GAC Pro Asp Val Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp 820 825 830	981
ATC GAG TTG GCG CAG ACC TTG CAG GCA GCC CCT GGG GAG GAG GAG GAG Ile Glu Leu Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Glu 835 840 845	1029
AAA GTG GAA GAG GTG CCA CAC CCA CTG GAT CGA GAC TAC CAG CTC CTC Lys Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu 850 855 860	1077
AGG TGC CAG CTT CAA CTG CTG GAC TCC GGG GAG TCC GAG TAC AAG GCA Arg Cys Gln Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala 865 870 875	1125
ATA CAG ACC TAC CTG AAA CAG ACT GGC AAC AGC TAC AGG TGC CCA AAC Ile Gln Thr Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn 880 885 890 895	1173
CTG CGG CAT GTT TGG AAA GTG AAC CGA GAA GGG GAG GGA GAC AGG TTC Leu Arg His Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe 900 905 910	1221
CAG GCC CAC TCC AAA CTG GGC AAT CGG AGG CTG CTG TGG CAC GGC ACC	1269

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AAT	GTG	GCC	GTG	GTG	GCT	GCC	ATC	CTC	ACC	AGT	GGG	CTC	CGA	ATC	ATG	1317	
Asn	Val	Ala	Val	Val	Ala	Ala	Ile	Leu	Thr	Ser	Gly	Leu	Arg	Ile	Met		
		930					935					940					
CCA	CAC	TCG	GGT	GGT	CGT	GTT	GGC	AAG	GGT	ATT	TAT	TTT	GCC	TCT	GAG	1365	
Pro	His	Ser	Gly	Gly	Arg	Val	Gly	Lys	Gly	Ile	Tyr	Phe	Ala	Ser	Glu		
		945				950					955						
AAC	AGC	AAG	TCA	GCT	GGC	TAT	GTT	ACC	ACC	ATG	CAC	TGT	GGG	GGC	CAC	1413	
Asn	Ser	Lys	Ser	Ala	Gly	Tyr	Val	Thr	Thr	Met	His	Cys	Gly	Gly	His		
960					965					970					975		
CAG	GTG	GGC	TAC	ATG	TTC	CTG	GGC	GAG	GTG	GCC	CTC	GGC	AAA	GAG	CAC	1461	
Gln	Val	Gly	Tyr	Met	Phe	Leu	Gly	Glu	Val	Ala	Leu	Gly	Lys	Glu	His		
				980					985					990			
CAC	ATC	ACC	ATC	GAT	GAC	CCC	AGC	TTG	AAG	AGT	CCA	CCC	CCT	GGC	TTT	1509	
His	Ile	Thr	Ile	Asp	Asp	Pro	Ser	Leu	Lys	Ser	Pro	Pro	Pro	Gly	Phe		
			995					1000						1005			
GAC	AGC	GTC	ATC	GCC	CGA	GGC	CAA	ACC	GAG	CCG	GAT	CCC	GCC	CAG	GAC	1557	
Asp	Ser	Val	Ile	Ala	Arg	Gly	Gln	Thr	Glu	Pro	Asp	Pro	Ala	Gln	Asp		
		1010					1015					1020					
ATT	GAA	CTT	GAA	CTG	GAT	GGG	CAG	CCG	GTG	GTG	GTG	CCC	CAA	GGC	CCG	1605	
Ile	Glu	Leu	Glu	Leu	Asp	Gly	Gln	Pro	Val	Val	Val	Pro	Gln	Gly	Pro		
	1025					1030					1035						
CCT	GTG	CAG	TGC	CCG	TCA	TTC	AAA	AGC	TCC	AGC	TTC	AGC	CAG	AGT	GAA	1653	
Pro	Val	Gln	Cys	Pro	Ser	Phe	Lys	Ser	Ser	Ser	Phe	Ser	Gln	Ser	Glu		
1040					1045				1050						1055		
TAC	CTC	ATA	TAC	AAG	GAG	AGC	CAG	TGT	CGC	CTG	CGC	TAC	CTG	CTG	GAG	1701	
Tyr	Leu	Ile	Tyr	Lys	Glu	Ser	Gln	Cys	Arg	Leu	Arg	Tyr	Leu	Leu	Glu		
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Ile	His	Leu															

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<212> PRT

<213> Mus musculus

<400> 8

Met	Ala	Pro	Lys	Arg	Lys	Ala	Ser	Val	Gln	Thr	Glu	Gly	Ser	Lys	Lys
1				5					10					15	

Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu

20					25					30						
Ala	Leu	Arg	Ala	Ala	Pro	Ala	Asp	Asn	Arg	Val	Ile	Arg	Val	Asp	Pro	
35					40					45						
Ser	Cys	Pro	Phe	Ser	Arg	Asn	Pro	Gly	Ile	Gln	Val	His	Glu	Asp	Tyr	
50					55					60						
Asp	Cys	Thr	Leu	Asn	Gln	Thr	Asn	Ile	Gly	Asn	Asn	Asn	Asn	Lys	Phe	
65					70					75					80	
Tyr	Ile	Ile	Gln	Leu	Leu	Glu	Glu	Gly	Ser	Arg	Phe	Phe	Cys	Trp	Asn	
85					90					95						
Arg	Trp	Gly	Arg	Val	Gly	Glu	Val	Gly	Gln	Ser	Lys	Met	Asn	His	Phe	
100					105					110						
Thr	Cys	Leu	Glu	Asp	Ala	Lys	Lys	Asp	Phe	Lys	Lys	Lys	Phe	Trp	Glu	
115					120					125						
Lys	Thr	Lys	Asn	Lys	Trp	Glu	Glu	Arg	Asp	Arg	Phe	Val	Ala	Gln	Pro	
130					135					140						
Asn	Lys	Tyr	Thr	Leu	Ile	Glu	Val	Gln	Gly	Glu	Ala	Glu	Ser	Gln	Glu	
145					150					155					160	
Ala	Val	Val	Lys	Ala	Leu	Ser	Pro	Gln	Val	Asp	Ser	Gly	Pro	Val	Arg	
165					170					175						
Thr	Val	Val	Lys	Pro	Cys	Ser	Leu	Asp	Pro	Ala	Thr	Gln	Asn	Leu	Ile	
180					185					190						
Thr	Asn	Ile	Phe	Ser	Lys	Glu	Met	Phe	Lys	Asn	Ala	Met	Thr	Leu	Met	
195					200					205						
Asn	Leu	Asp	Val	Lys	Lys	Met	Pro	Leu	Gly	Lys	Leu	Thr	Lys	Gln	Gln	
210					215					220						
Ile	Ala	Arg	Gly	Phe	Glu	Ala	Leu	Glu	Ala	Leu	Glu	Glu	Ala	Met	Lys	
225					230					235					240	
Asn	Pro	Thr	Gly	Asp	Gly	Gln	Ser	Leu	Glu	Glu	Leu	Ser	Ser	Cys	Phe	
245					250					255						
Tyr	Thr	Val	Ile	Pro	His	Asn	Phe	Gly	Arg	Ser	Arg	Pro	Pro	Pro	Ile	
260					265					270						
Asn	Ser	Pro	Asp	Val	Leu	Gln	Ala	Lys	Lys	Asp	Met	Leu	Leu	Val	Leu	
275					280					285						
Ala	Asp	Ile	Glu	Leu	Ala	Gln	Thr	Leu	Gln	Ala	Ala	Pro	Gly	Glu	Glu	
290					295					300						
Glu	Glu	Lys	Val	Glu	Glu	Val	Pro	His	Pro	Leu	Asp	Arg	Asp	Tyr	Gln	
305					310					315					320	

Leu Leu Arg Cys Gln Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr
 325 330 335

Lys Ala Ile Gln Thr Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys
 340 345 350

Pro Asn Leu Arg His Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp
 355 360 365

Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His
 370 375 380

Gly Thr Asn Val Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg
 385 390 395 400

Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala
 405 410 415

Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly
 420 425 430

Gly His Gln Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys
 435 440 445

Glu His His Ile Thr Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro
 450 455 460

Gly Phe Asp Ser Val Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala
 465 470 475 480

Gln Asp Ile Glu Leu Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln
 485 490 495

Gly Pro Pro Val Gln Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln
 500 505 510

Ser Glu Tyr Leu Ile Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu
 515 520 525

Leu Glu Ile His Leu
 530

<210> 9

<211> 1587

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> 1..1584

<400> 9

ATG GCT CCA AAA CGA AAG GCC TCT GTG CAG ACT GAG GGC TCC AAG AAG	48
Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys	
535 540 545	
CAG CGA CAA GGG ACA GAG GAG GAG GAC AGC TTC CGG TCC ACT GCC GAG	96
Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu	
550 555 560 565	
GCT CTC AGA GCA GCA CCT GCT GAT AAT CGG GTC ATC CGT GTG GAC CCC	144
Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro	
570 575 580	
TCA TGT CCA TTC AGC CGG AAC CCC GGG ATA CAG GTC CAC GAG GAC TAT	192
Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr	
585 590 595	
GAC TGT ACC CTG AAC CAG ACC AAC ATC GGC AAC AAC AAC AAC AAG TTC	240
Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe	
600 605 610	
TAT ATT ATC CAA CTG CTG GAG GAG GGT AGT CGC TTC TTC TGC TGG AAT	288
Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn	
615 620 625	
CGC TGG GGC CGC GTG GGA GAG GTG GGC CAG AGC AAG ATG AAC CAC TTC	336
Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe	
630 635 640 645	
ACC TGC CTG GAA GAT GCA AAG AAG GAC TTT AAG AAG AAA TTT TGG GAG	384
Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu	
650 655 660	
AAG ACT AAA AAC AAA TGG GAG GAG CGG GAC CGT TTT GTG GCC CAG CCC	432
Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro	
665 670 675	
AAC AAG TAC ACA CTT ATA GAA GTC CAG GGA GAA GCA GAG AGC CAA GAG	480
Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu	
680 685 690	
GCT GTA GTG AAG GTG GAC AGC GGC CCT GTG AGG ACC GTG GTC AAG CCC	528
Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro	
695 700 705	
TGC TCC CTA GAC CCT GCC ACC CAG AAC CTT ATC ACC AAC ATC TTC AGC	576
Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser	
710 715 720 725	
AAA GAG ATG TTC AAG AAC GCA ATG ACC CTC ATG AAC CTG GAT GTG AAG	624
Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys	
730 735 740	
AAG ATG CCC TTG GGA AAG CTG ACC AAG CAG CAG ATT GCC CGT GGC TTC	672
Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala Arg Gly Phe	

745	750	755	
GAG GCC TTG GAA GCT CTA Glu Ala Leu Glu Ala Leu 760	GAG GAG GCC ATG AAA AAC Glu Glu Ala Met Lys Asn 765	CCC ACA GGG GAT Pro Thr Gly Asp 770	720
GGC CAG AGC CTG GAA GAG CTC Gly Gln Ser Leu Glu Glu Leu 775	TCC TCC TGC TTC TAC ACT Ser Ser Cys Phe Tyr Thr 780	GTC ATC CCA Val Ile Pro 785	768
CAC AAC TTC GGC CGC AGC CGA His Asn Phe Gly Arg Ser Arg 790	CCC CCG CCC ATC AAC TCC Pro Pro Pro Ile Asn Ser 795	CCT GAT GTG Pro Asp Val 800	816
CTT CAG GCC AAG AAG GAC ATG Leu Gln Ala Lys Lys Asp Met 810	CTG CTG GTG CTA GCG GAC Leu Leu Val Leu Ala Asp 815	ATC GAG TTG Ile Glu Leu 820	864
GCG CAG ACC TTG CAG GCA GCC Ala Gln Thr Leu Gln Ala Ala 825	CCT GGG GAG GAG GAG GAG Pro Gly Glu Glu Glu Glu 830	AAA GTG GAA Lys Val Glu 835	912
GAG GTG CCA CAC CCA CTG GAT Glu Val Pro His Pro Leu Asp 840	CGA GAC TAC CAG CTC CTC Arg Asp Tyr Gln Leu Leu 845	AGG TGC CAG Arg Cys Gln 850	960
CTT CAA CTG CTG GAC TCC GGG Leu Gln Leu Leu Asp Ser Gly 855	GAG TCC GAG TAC AAG GCA Glu Ser Glu Tyr Lys Ala 860	ATA CAG ACC Ile Gln Thr 865	1008
TAC CTG AAA CAG ACT GGC AAC Tyr Leu Lys Gln Thr Gly Asn 870	AGC TAC AGG TGC CCA AAC Ser Tyr Arg Cys Pro Asn 875	CTG CGG CAT Leu Arg His 885	1056
GTT TGG AAA GTG AAC CGA GAA Val Trp Lys Val Asn Arg Glu 890	GGG GAG GGA GAC AGG TTC Gly Glu Gly Asp Arg Phe 895	CAG GCC CAC Gln Ala His 900	1104
TCC AAA CTG GGC AAT CGG AGG Ser Lys Leu Gly Asn Arg Arg 905	CTG CTG TGG CAC GGC ACC Leu Leu Trp His Gly Thr 910	AAT GTG GCC Asn Val Ala 915	1152
GTG GTG GCT GCC ATC CTC ACC Val Val Ala Ala Ile Leu Thr 920	AGT GGG CTC CGA ATC ATG Ser Gly Leu Arg Ile Met 925	CCA CAC TCG Pro His Ser 930	1200
GGT GGT CGT GTT GGC AAG GGT Gly Gly Arg Val Gly Lys Gly 935	ATT TAT TTT GCC TCT GAG Ile Tyr Phe Ala Ser Glu 940	AAC AGC AAG Asn Ser Lys 945	1248
TCA GCT GGC TAT GTT ACC ACC Ser Ala Gly Tyr Val Thr Thr 950	ATG CAC TGT GGG GGC CAC Met His Cys Gly Gly His 955	CAG GTG GGC Gln Val Gly 960	1296

TAC ATG TTC CTG GGC GAG GTG GCC CTC GGC AAA GAG CAC CAC ATC ACC	1344
Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His His Ile Thr	
970 975 980	
ATC GAT GAC CCC AGC TTG AAG AGT CCA CCC CCT GGC TTT GAC AGC GTC	1392
Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val	
985 990 995	
ATC GCC CGA GGC CAA ACC GAG CCG GAT CCC GCC CAG GAC ATT GAA CTT	1440
Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp Ile Glu Leu	
1000 1005 1010	
GAA CTG GAT GGG CAG CCG GTG GTG GTG CCC CAA GGC CCG CCT GTG CAG	1488
Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln	
1015 1020 1025	
TGC CCG TCA TTC AAA AGC TCC AGC TTC AGC CAG AGT GAA TAC CTC ATA	1536
Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile	
1030 1035 1040 1045	
TAC AAG GAG AGC CAG TGT CGC CTG CGC TAC CTG CTG GAG ATT CAC CTC	1584
Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu	
1050 1055 1060	
TAA	1587

<210> 10
 <211> 528
 <212> DNA
 <213> Mus musculus

<400> 10

Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys	
1 5 10 15	
Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu	
20 25 30	
Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro	
35 40 45	
Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr	
50 55 60	
Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe	
65 70 75 80	
Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn	
85 90 95	
Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe	

100					105					110					
Thr	Cys	Leu	Glu	Asp	Ala	Lys	Lys	Asp	Ph	Lys	Lys	Lys	Phe	Trp	Glu
		115						120					125		
Lys	Thr	Lys	Asn	Lys	Trp	Glu	Glu	Arg	Asp	Arg	Phe	Val	Ala	Gln	Pro
	130					135					140				
Asn	Lys	Tyr	Thr	Leu	Ile	Glu	Val	Gln	Gly	Glu	Ala	Glu	Ser	Gln	Glu
145					150					155					160
Ala	Val	Val	Lys	Val	Asp	Ser	Gly	Pro	Val	Arg	Thr	Val	Val	Lys	Pro
				165					170					175	
Cys	Ser	Leu	Asp	Pro	Ala	Thr	Gln	Asn	Leu	Ile	Thr	Asn	Ile	Phe	Ser
			180					185					190		
Lys	Glu	Met	Phe	Lys	Asn	Ala	Met	Thr	Leu	Met	Asn	Leu	Asp	Val	Lys
		195					200					205			
Lys	Met	Pro	Leu	Gly	Lys	Leu	Thr	Lys	Gln	Gln	Ile	Ala	Arg	Gly	Phe
	210					215					220				
Glu	Ala	Leu	Glu	Ala	Leu	Glu	Glu	Ala	Met	Lys	Asn	Pro	Thr	Gly	Asp
225					230					235					240
Gly	Gln	Ser	Leu	Glu	Glu	Leu	Ser	Ser	Cys	Phe	Tyr	Thr	Val	Ile	Pro
			245						250					255	
His	Asn	Phe	Gly	Arg	Ser	Arg	Pro	Pro	Pro	Ile	Asn	Ser	Pro	Asp	Val
			260					265					270		
Leu	Gln	Ala	Lys	Lys	Asp	Met	Leu	Leu	Val	Leu	Ala	Asp	Ile	Glu	Leu
		275					280					285			
Ala	Gln	Thr	Leu	Gln	Ala	Ala	Pro	Gly	Glu	Glu	Glu	Glu	Lys	Val	Glu
		290				295						300			
Glu	Val	Pro	His	Pro	Leu	Asp	Arg	Asp	Tyr	Gln	Leu	Leu	Arg	Cys	Gln
305					310					315					320
Leu	Gln	Leu	Leu	Asp	Ser	Gly	Glu	Ser	Glu	Tyr	Lys	Ala	Ile	Gln	Thr
			325						330					335	
Tyr	Leu	Lys	Gln	Thr	Gly	Asn	Ser	Tyr	Arg	Cys	Pro	Asn	Leu	Arg	His
			340					345					350		
Val	Trp	Lys	Val	Asn	Arg	Glu	Gly	Glu	Gly	Asp	Arg	Phe	Gln	Ala	His
		355					360					365			
Ser	Lys	Leu	Gly	Asn	Arg	Arg	Leu	Leu	Trp	His	Gly	Thr	Asn	Val	Ala
		370				375					380				
Val	Val	Ala	Ala	Ile	Leu	Thr	Ser	Gly	Leu	Arg	Ile	Met	Pro	His	Ser
385					390					395					400

Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys
 405 410 415

Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His Gln Val Gly
 420 425 430

Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His His Ile Thr
 435 440 445

Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val
 450 455 460

Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp Ile Glu Leu
 465 470 475 480

Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln
 485 490 495

Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile
 500 505 510

Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu
 515 520 525

<210> 11

<211> 18

<212> PRT

<213> artificial sequence

<220>

<223> NAD⁺ binding domain

<220>

<221> VARIANT

<222> 2..6

<223> amino acid residues 2 through 6 may be any amino acid, and residues 3 to 6 may be present or absent

<220>

<221> VARIANT

<222> 7

<223> amino acid residue 7 is either Ser or Thr

<400> 11

Pro Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Gly Lys Gly Ile Tyr
 5 10 15

Phe Ala

<210> 12

<211> 25
 <212> PRT
 <213> artificial sequence

<220>
 <223> NAD⁺ binding domain

<220>
 <221> VARIANT
 <222> 1, 14
 <223> amino acid residues 1 and 14 are either Ser or Thr

<220>
 <221> VARIANT
 <222> 2, 9..13, 16..18
 <223> amino acid residues 2, 9 to 13 and 16 to 18 may be any amino acid;
 residues 10 to 13 may be present or absent

<220>
 <221> VARIANT
 <222> 6
 <223> amino acid residue 6 is either Ile or Val

<400> 12

Xaa	Xaa	Gly	Leu	Arg	Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa
				5				10					15	

Xaa	Xaa	Gly	Lys	Gly	Ile	Tyr	Phe	Ala
			20					25

<210> 13
 <211> 49
 <212> PRT
 <213> artificial sequence

<220>
 <223> NAD⁺ binding domain

<220>
 <221> VARIANT
 <222> 6, 16, 29
 <223> amino acid residues 6, 16 and 29 are either Ser or Thr

<220>
 <221> VARIANT
 <222> 7..13, 17, 22, 31..33,41..43,48
 <223> amino acid residues 7 to 13, 17, 22, 24 to 28, 31 to 33, 41 to 43 and 48
 may be any amino acid; residues 25 to 28 may be present or absent

<220>
 <221> VARIANT

<222> 21

<223> amino acid residue 21 is either Ile or Val

<400> 13

Leu Leu Trp His Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Leu Xaa
5 10 15

Xaa Gly Leu Arg Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa
20 25 30

Xaa Gly Lys Gly Ile Tyr Phe Ala Xaa Xaa Xaa Ser Lys Ser Ala Xaa
35 40 45

Tyr

<210> 14

<211> 22

<212> PRT

<213> artificial sequence

<220>

<223> leucine zipper motif

<220>

<221> VARIANT

<222> 1

<223> amino acid residue 1 is either Leu or Val

<220>

<221> VARIANT

<222> 2..7, 9..14, 16..20

<223> amino acid residues 2 to 7, 9 to 14 and 16 to 20 may be any amino acid

<400> 14

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa
5 10 15

Xaa Xaa Xaa Xaa Xaa Leu
20

<210> 15

<211> 37

<212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 1

<220>

<221> VARIANT

<222> 21

<223> Xaa is either Asp or Glu

<220>

<221> VARIANT

<222> 22..32

<223> amino acid residues 22 to 32 may be any amino acid; residue 32 may be present or absent

<400> 15

Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Tyr Xaa Xaa
5 10 15

Gln Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Trp Gly Arg Val Gly
35

<210> 16

<211> 29

<212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 2

<220>

<221> VARIANT

<222> 2..4, 6, 8..11, 14, 16, 18..22, 24..26, 28

<223> amino acid residues 2 to 4, 6, 8 to 11, 14, 16, 18 to 22, 24 to 26 and 28 may be any amino acid

<400> 16

Ala Xaa Xaa Xaa Phe Xaa Lys Xaa Xaa Xaa Xaa Lys Thr Xaa Asn Xaa
5 10 15

Trp Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Pro Xaa Lys
20 25

<210> 17

<211> 44

<212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 3

<220>

<221> VARIANT

<222> 2, 5..6, 8..16, 18..27, 33..35, 38..43

<223> amino acid residues 2, 5 to 6, 8 to 16, 18 to 27, 33 to 35, and 38 to 43 may be any amino acid

<220>

<221> VARIANT

<222> 4

<223> amino acid residue 4 is either Ile or Leu

<400> 17

Gln	Xaa	Leu	Xaa	Xaa	Xaa	Ile	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				5					10						15		
Met	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Leu	Gly	Lys	Leu		
			20					25					30				
Xaa	Xaa	Xaa	Gln	Ile	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu					
			35					40									

<210> 18

<211> 15

<212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 4

<220>

<221> VARIANT

<222> 4, 8, 11..13

<223> amino acid residues 4, 8 and 11 to 13 may be any amino acid

<400> 18

Phe	Tyr	Thr	Xaa	Ile	Pro	His	Xaa	Phe	Gly	Xaa	Xaa	Xaa	Pro	Pro
				5					10				15	

<210> 19

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 5

<220>

<221> VARIANT

<222> 2..4, 6..7, 9, 13, 15..16

<223> amino acid residues 2 to 4, 6 to 7, 9, 13 and 15 to 16 may be any amino acid

<400>

Lys Xaa Xaa Xaa Leu Xaa Xaa Leu Xaa Asp Ile Glu Xaa Ala Xaa Xaa
 5 10 15

Leu

<210> 20

<211> 11

<212> PRT

<213> artificial sequence

<200>

<223> part-sequence motif 6

<220>

<221> VARIANT

<222> 2..4, 6

<223> amino acid residues 2 to 4 and 6 may be any amino acid

<400> 20

Gly Xaa Xaa Xaa Leu Xaa Glu Val Ala Leu Gly
 5 10

<210> 21

<211> 28

<212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 7

<220>

<221> VARIANT

<222> 2..3, 5..8, 10..12, 14..22, 24, 26..27

<223> amino acid residues 2 to 3, 5 to 8, 10 to 12, 14 to 22, 24, 26 to 27 may be any amino acid; residues 21 and 22 may be present or absent

<400> 21

Gly Xaa Xaa Ser Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Pro Xaa Xaa Xaa
 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Gly Xaa Xaa Val
 20 25

<210> 22

<211> 16

<212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 8

<220>

<221> VARIANT

<222> 2

<223> amino acid residue 2 is either Tyr or Phe

<220>

<221> VARIANT

<222> 3..4, 6..8, 10..13

<223> amino acid residues 3 to 4, 6 to 8 and 10 to 13 may be any amino acid

<400> 22

Glu	Xaa	Xaa	Xaa	Tyr	Xaa	Xaa	Xaa	Gln	Xaa	Xaa	Xaa	Xaa	Tyr	Leu	Leu
				5				10						15	

<210> 23

<211> 20

<212> PRT

<213> artificial sequence

<220>

<223> synthetic sequence for antibody production

<400> 23

Met	Ala	Ala	Arg	Arg	Arg	Arg	Ser	Thr	Gly	Gly	Gly	Arg	Ala	Arg	Ala
			5						10					15	

Leu	Asn	Glu	Ser
			20

<210> 24

<211> 20

<212> PRT

<213> artificial sequence

<220>

<223> synthetic sequence for antibody production

<400> 24

Lys	Thr	Glu	Leu	Gln	Ser	Pro	Glu	His	Pro	Leu	Asp	Gln	His	Tyr	Arg
				5				10						15	

Asn	Leu	His	Cys
			20

<210> 25
 <211> 21
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic sequence for antibody production

<400> 25

Cys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser Thr
 5 10 15

Ala Glu Ala Leu Lys
 20

<210> 26
 <211> 20
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic sequence for antibody production

<400> 26

Cys Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu
 5 10 15

Glu Ala Leu Lys
 20

<210> 27
 <211> 19
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic sequence for antibody production

<400> 27

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu
 5 10 15

Ala Leu Lys

<210> 28
 <211> 19
 <212> PRT
 <213> Mus musculus

<400>28

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu
 5 10 15

Ala Met Lys

<210> 29

<211> 7

<212> PRT

<213> artificial sequence

<220>

<223> NAD⁺ binding domain

<220>

<221> VARIANT

<222> 2..4

<223> amino acid residues 2 to 4 may be any amino acid residue

Gly Xaa Xaa Xaa Gly Lys Gly
 5

<210> 30

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> PARP zinc finger sequence motif

<220>

<221> VARIANT

<222> 2..3, 5..34, 36..37

<223> amino acid residues 2 to 3, 5 to 34 and 36 to 37 may be any amino acid residue; residues 33 and 34 may be present or absent

Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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